regions. Several of these were chosen as candidates for probe design. Using the DNA sequences of cloned genes from *Corynebacterium* , a codon preference table was derived. From this a backtranslation was performed resulting in the most likely DNA sequence for the protein region of interest.

B2

Please replace paragraph 0128 with the following rewritten paragraph:

Two of the resulting probes (TM63 and TM74), shown in Table 1, below, were labeled, mixed, and used to screen the above genomic library. Oligos were labeled with γ^{32}PATP using T4 polynucleotide kinase as described (Ausubel, *et al*, eds, 1994. "Current Protocols in Molecular Biology," John Wiley and Sons, Inc.,) and cleaned up using Elutips (Schleicher & Schuell). Hybridization of duplicate filters was carried out in a Bellco hybridization oven at 37°C using the SSPE protocol as described (Ausubel, *et al.*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994). Filters were washed in 6X SSC with 0.5%SDS (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) at 37°C. Filters were then washed at successively higher temperatures in 3 M TMAC (Ausubel, *et al*, eds, "Current Protocols in Molecular Biology," John Wiley and Sons, Inc., 1994) until very little radioactivity could be detected with a survey meter (generally 45 - 55°C). Upon exposure to X-Ray film (Kodak X-Omat), colonies which were evident on both replicate filters were picked with a wooden toothpick and transferred to a fresh nylon filter overlaid onto an LB/ampicillin plate. This procedure was repeated until a homogeneous population was achieved.

B3

Table 1: oligonucleotides (SEQ ID NOS 13-31, respectively, in order of appearance) with DNA sequence and approximate coordinates relative to the ATG start codon.

Name	Length	Sequence (5' to 3')	Coordinates
TM63	30	CGCGTTCAGGACGCATACTCCGTTCGCTGC	838-867
TM74	24	GCCCATGGAAACGTGGTCTTCCTG	1370-1393
TM85	21	ATCATCATGCCCGAGTCCACA	1156-1176

TM87	21	GCCATCAGGAAGACCACGTTT	990-971
TM89	20	ATGCAGGAAGACCACGTTTC	1246-1265
TM91	21	ATCGAGGTCCGCCAATGCCAT	648-628
TM92	18	ACCGGAGCAGCCCAGTGA	441-424
TM93	20	TGCTTGAAGTATTGCGCCAG	1403-1422
TM94	18	GATCCTCGGGTGCGATGT	226-209
TM95	18	ATGCTGATCGGGCTTCGT	92-74
TM96	27	ATTTGATTCATATGGCTTCCGCTCCTC	-11- +16
TM97	28	ATCTTGGATCCGAACATGGTGCGTTGCA	Beyond C-Terminus
TM98	18	AGCACCAGAT CGATGCAC	128-145
TM99	18	TGGCATGGGTGAACCGGT	267-284
TM101	18	ATCAGCGTTGAAGCCCAG	682–699
TM103	18	ACGTGCTGGACTTCCTTG	1019-1036
TM105	18	GTGCATAAGGCCCTCGAA	1501-1518
TM106	18	GAGCTTCGAGGGCCTTAT	1522-1505
TM109	18	CGAGCAACGCAGCGAGTA	870–853

B3

Please replace paragraph 0133 with the following paragraph:

B4

HAL from a bacterium from the family *Corynebacteriaceae* that had been partially purified using ammonium sulfate and DEAE - Sephadex was resolved by SDS-PAGE. The separated material was electrophoretically transferred to Immobilon-P and stained with Coomassie Brilliant Blue. The major band of 55 000 daltons was excised and subjected to